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Winkler, U.
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GENERALIGN - Multiple Sequence Alignment Program
Release 5.4

Solution Parameters:

Nucleic Alphabet	= Identity
Output Line Length	= 80
Compress	= Off
HiStorage	= Off
Randomization	= Off
AMINO-Rees-Length	= 2
Direction-Weight	= 5.00
Length-factor	= 0
Matching-weight	= 1.00
NUCLEIC-Rees-Length	= 4
Spread-factor	= 50

Clustered order of selected sequences:

3. US-09-303-040-5 (1-1080)
80. US-09-303-510-5 (1-1080)

Region Alignment: (listed in clustered order)

[illegible]

US-09-303-	367	AGATCAAGGACAAAGGACCAATATCACTGTTTCAATCAATTAAGAGGCCCAAGAGCATAG
US-09-303-	367	AGATCAAGGACAAAGGACCAATATCACTGTTTCAATCAATTAAGAGGCCCAAGAGCATAG
US-09-303-	367	AGATCAAGGACAAAGGACCAATATCACTGTTTCAATCAATTAAGAGGCCCAAGAGCATAG
consensus		AGATCAAGGACAAAGGACCAATATCACTGTTTCAATCAATTAAGAGGCCCAAGAGCATAG
US-09-303-	428	TCCCATGCAACCAATGAGTTCCTGACCTTAACAGTGCTTGCTAACTTCACTGCACTGAAATTT
US-09-303-	428	TCCCATGCAACCAATGAGTTCCTGACCTTAACAGTGCTTGCTAACTTCACTGCACTGAAATTT
US-09-303-	428	TCCCATGCAACCAATGAGTTCCTGACCTTAACAGTGCTTGCTAACTTCACTGCACTGAAATTT
consensus		TCCCATGCAACCAATGAGTTCCTGACCTTAACAGTGCTTGCTAACTTCACTGCACTGAAATTT
US-09-303-	489	ACAGTAACTTCAATATGAAACAGAAATTCTGCGATCTAAATTTGACCTGCTCATCTATAC
US-09-303-	489	ACAGTAACTTCAATATGAAACAGAAATTCTGCGATCTAAATTTGACCTGCTCATCTATAC
US-09-303-	489	ACAGTAACTTCAATATGAAACAGAAATTCTGCGATCTAAATTTGACCTGCTCATCTATAC
consensus		ACAGTAACTTCAATATGAAACAGAAATTCTGCGATCTAAATTTGACCTGCTCATCTATAC
US-09-303-	550	AAAGTTAACCCGAAACCTAAGAGAGATGATTTTCAGACTAAACATGAGAAATTCACACTAAT
US-09-303-	550	AAAGTTAACCCGAAACCTAAGAGAGATGATTTTCAGACTAAACATGAGAAATTCACACTAAT
US-09-303-	550	AAAGTTAACCCGAAACCTAAGAGAGATGATTTTCAGACTAAACATGAGAAATTCACACTAAT
consensus		AAAGTTAACCCGAAACCTAAGAGAGATGATTTTCAGACTAAACATGAGAAATTCACACTAAT
US-09-303-	611	GTATGATACCTCATATGAGAAATCTCAAAATATATGACAGAACTGTACAAAGCTTCTATCT
US-09-303-	611	GTATGATACCTCATATGAGAAATCTCAAAATATATGACAGAACTGTACAAAGCTTCTATCT
US-09-303-	611	GTATGATACCTCATATGAGAAATCTCAAAATATATGACAGAACTGTACAAAGCTTCTATCT
consensus		GTATGATACCTCATATGAGAAATCTCAAAATATATGACAGAACTGTACAAAGCTTCTATCT
US-09-303-	672	AGCTTGCCTTTTCAGTCCCTGAGAGCAACAATGAGAGCGTCTTTTGTGCCCTGAAACTGAG
US-09-303-	672	AGCTTGCCTTTTCAGTCCCTGAGAGCAACAATGAGAGCGTCTTTTGTGCCCTGAAACTGAG
US-09-303-	672	AGCTTGCCTTTTCAGTCCCTGAGAGCAACAATGAGAGCGTCTTTTGTGCCCTGAAACTGAG
consensus		AGCTTGCCTTTTCAGTCCCTGAGAGCAACAATGAGAGCGTCTTTTGTGCCCTGAAACTGAG
US-09-303-	733	AGACATGAGATGCTGCTCTCCCTCACTTTCATATATGATGCAAACTAAGAGTAAAG
US-09-303-	733	AGACATGAGATGCTGCTCTCCCTCACTTTCATATATGATGCAAACTAAGAGTAAAG
US-09-303-	733	AGACATGAGATGCTGCTCTCCCTCACTTTCATATATGATGCAAACTAAGAGTAAAG
consensus		AGACATGAGATGCTGCTCTCCCTCACTTTCATATATGATGCAAACTAAGAGTAAAG
US-09-303-	794	CCCTGACAAAGGCGACTTCTCTGAGATTCGCGACTGTACTTGTAAATGTTTGTGTTTTGT
US-09-303-	794	CCCTGACAAAGGCGACTTCTCTGAGATTCGCGACTGTACTTGTAAATGTTTGTGTTTTGT
US-09-303-	794	CCCTGACAAAGGCGACTTCTCTGAGATTCGCGACTGTACTTGTAAATGTTTGTGTTTTGT
consensus		CCCTGACAAAGGCGACTTCTCTGAGATTCGCGACTGTACTTGTAAATGTTTGTGTTTTGT
US-09-303-	855	GGAATGATGTCCTTTAAACACTAAGAAAGAGAAAGAGAGCAAGCTGGCCCTCTCTCATG
US-09-303-	855	GGAATGATGTCCTTTAAACACTAAGAAAGAGAAAGAGAGCAAGCTGGCCCTCTCTCATG
US-09-303-	855	GGAATGATGTCCTTTAAACACTAAGAAAGAGAAAGAGAGCAAGCTGGCCCTCTCTCATG
consensus		GGAATGATGTCCTTTAAACACTAAGAAAGAGAAAGAGAGCAAGCTGGCCCTCTCTCATG
US-09-303-	916	AATGTAAACCATCAAAAGGAGAGAAAGAGAGCAACAGACCAACGAAGAGATACATAT
US-09-303-	916	AATGTAAACCATCAAAAGGAGAGAAAGAGAGCAACAGACCAACGAAGAGATACATAT
US-09-303-	916	AATGTAAACCATCAAAAGGAGAGAAAGAGAGCAACAGACCAACGAAGAGATACATAT
consensus		AATGTAAACCATCAAAAGGAGAGAAAGAGAGCAACAGACCAACGAAGAGATACATAT
US-09-303-	977	CGACGTACTGAGAGCTGTATGAAACCGAGGTGTATCAATTTGAGAGACAGCTCAGAG

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US-09-303- 977 CCACGTACCTGAGATCTGATGAGCCGAGGTGTTCACATTTGAGGACAGCTCAGGG
consensus CCACGTACCTGAGATCTGATGAGCCGAGGTGTTCACATTTGAGGACAGCTCAGGG

US-09-303- 1038 GACAAATTCATGCGAAATGCTGCTTGGCTGCTGACAT
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US-09-303- 1038 GACAAATTCATGCGAAATGCTGCTTGGCTGCTGACAT

consensus GACAAATTCATGCGAAATGCTGCTTGGCTGCTGACAT

Alignment score = 1080.00

Scoring matrix:

	3	80
3	1080	
80		

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